

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/558, 149A
Source: JFW16
Date Processed by STIC: 03/14/2006

ENTERED



IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/558,149A

DATE: 03/14/2006
 TIME: 11:52:44

Input Set : A:\980232_1.TXT
 Output Set: N:\CRF4\03142006\I558149A.raw

4 <110> APPLICANT: NICOLAIDES, NICHOLAS
 5 VOGELSTEIN, BERT
 6 KINZLER, KINZLER
 8 <120> TITLE OF INVENTION: A METHOD FOR GENERATING HYPERMUTABLE
 9 ORGANISMS
 11 <130> FILE REFERENCE: 01107.00004
 13 <140> CURRENT APPLICATION NUMBER: 09/558149A
 14 <141> CURRENT FILING DATE: 2000-04-26
 16 <150> PRIOR APPLICATION NUMBER: 09/059461
 17 <151> PRIOR FILING DATE: 1998-04-14
 19 <160> NUMBER OF SEQ ID NOS: 8
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2771
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (25)...(2610)
 32 <400> SEQUENCE: 1
 33 cgaggcggat cgggtgttgc atcc atg gag cga gct gag agc tcg agt aca 51
 34 Met Glu Arg Ala Glu Ser Ser Ser Thr
 35 1 5
 37 gaa cct gct aag gcc atc aaa cct att gat cgg aag tca gtc cat cag 99
 38 Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln
 39 10 15 20 25
 41 att tgc tct ggg cag gtg gta ctg agt cta agc act gcg gta aag gag 147
 42 Ile Cys Ser Gly Gln Val Val Leu Ser Leu Ser Thr Ala Val Lys Glu
 43 30 35 40
 45 tta gta gaa aac agt ctg gat gct ggt gcc act aat att gat cta aag 195
 46 Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn Ile Asp Leu Lys
 47 45 50 55
 49 ctt aag gac tat gga gtg gat ctt att gaa gtt tca gac aat gga tgt 243
 50 Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser Asp Asn Gly Cys
 51 60 65 70
 53 ggg gta gaa gaa aac ttc gaa ggc tta act ctg aaa cat cac aca 291
 54 Gly Val Glu Glu Asn Phe Glu Gly Leu Thr Leu Lys His His Thr
 55 75 80 85
 57 tct aag att caa gag ttt gcc gac cta act cag gtt gaa act ttt ggc 339
 58 Ser Lys Ile Gln Glu Phe Ala Asp Leu Thr Gln Val Glu Thr Phe Gly
 59 90 95 100 105
 61 ttt cgg ggg gaa gct ctg agc tca ctt tgt gca ctg agc gat gtc acc 387
 62 Phe Arg Gly Glu Ala Leu Ser Ser Leu Cys Ala Leu Ser Asp Val Thr

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63	110	115	120	
65	att tct acc tgc cac gca tcg gcg aag gtt gga act cga ctg atg ttt			435
66	Ile Ser Thr Cys His Ala Ser Ala Lys Val Gly Thr Arg Leu Met Phe			
67	125	130	135	
69	gat cac aat ggg aaa att atc cag aaa acc ccc tac ccc cgc ccc aga			483
70	Asp His Asn Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg			
71	140	145	150	
73	ggg acc aca gtc agc gtg cag cag tta ttt tcc aca cta cct gtg cgc			531
74	Gly Thr Thr Val Ser Val Gln Gln Leu Phe Ser Thr Leu Pro Val Arg			
75	155	160	165	
77	cat aag gaa ttt caa agg aat att aag aag gag tat gcc aaa atg gtc			579
78	His Lys Glu Phe Gln Arg Asn Ile Lys Lys Glu Tyr Ala Lys Met Val			
79	170	175	180	185
81	cag gtc tta cat gca tac tgt atc att tca gca ggc atc cgt gta agt			627
82	Gln Val Leu His Ala Tyr Cys Ile Ile Ser Ala Gly Ile Arg Val Ser			
83	190	195	200	
85	tgc acc aat cag ctt gga caa gga aaa cga cag cct gtg gta tgc aca			675
86	Cys Thr Asn Gln Leu Gly Gln Gly Lys Arg Gln Pro Val Val Cys Thr			
87	205	210	215	
89	ggt gga agc ccc agc ata aag gaa aat atc ggc tct gtg ttt ggg cag			723
90	Gly Gly Ser Pro Ser Ile Lys Glu Asn Ile Gly Ser Val Phe Gly Gln			
91	220	225	230	
93	aag cag ttg caa agc ctc att cct ttt gtt cag ctg ccc cct agt gac			771
94	Lys Gln Leu Gln Ser Leu Ile Pro Phe Val Gln Leu Pro Pro Ser Asp			
95	235	240	245	
97	tcc gtg tgt gaa gag tac ggt ttg agc tgt tcg gat gct ctg cat aat			819
98	Ser Val Cys Glu Glu Tyr Gly Leu Ser Cys Ser Asp Ala Leu His Asn			
99	250	255	260	265
101	ctt ttt tac atc tca ggt ttc att tca caa tgc acg cat gga gtt gga			867
102	Leu Phe Tyr Ile Ser Gly Phe Ile Ser Gln Cys Thr His Gly Val Gly			
103	270	275	280	
105	agg agt tca aca gac aga cag ttt ttc ttt atc aac cgg cgg cct tgt			915
106	Arg Ser Ser Thr Asp Arg Gln Phe Phe Phe Ile Asn Arg Arg Pro Cys			
107	285	290	295	
109	gac cca gca aag gtc tgc aga ctc gtg aat gag gtc tac cac atg tat			963
110	Asp Pro Ala Lys Val Cys Arg Leu Val Asn Glu Val Tyr His Met Tyr			
111	300	305	310	
113	aat cga cac cag tat cca ttt gtt gtt ctt aac att tct gtt gat tca			1011
114	Asn Arg His Gln Tyr Pro Phe Val Val Leu Asn Ile Ser Val Asp Ser			
115	315	320	325	
117	gaa tgc gtt gat atc aat gtt act cca gat aaa agg caa att ttg cta			1059
118	Glu Cys Val Asp Ile Asn Val Thr Pro Asp Lys Arg Gln Ile Leu Leu			
119	330	335	340	345
121	caa gag gaa aag ctt ttg ttg gca gtt tta aag acc tct ttg ata gga			1107
122	Gln Glu Glu Lys Leu Leu Ala Val Leu Lys Thr Ser Leu Ile Gly			
123	350	355	360	
125	atg ttt gat agt gat gtc aac aag cta aat gtc agt cag cag cca ctg			1155
126	Met Phe Asp Ser Asp Val Asn Lys Leu Asn Val Ser Gln Gln Pro Leu			
127	365	370	375	

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129	ctg	gat	gtt	gaa	ggt	aac	tta	ata	aaa	atg	cat	gca	gct	gat	ttg	gaa	1203
130	Leu	Asp	Val	Glu	Gly	Asn	Leu	Ile	Lys	Met	His	Ala	Ala	Asp	Leu	Glu	
131	380			385						390							
133	aag	ccc	atg	gta	gaa	aag	cag	gat	caa	tcc	cct	tca	tta	agg	act	gga	1251
134	Lys	Pro	Met	Val	Glu	Lys	Gln	Asp	Gln	Ser	Pro	Ser	Leu	Arg	Thr	Gly	
135	395			400						405							
137	gaa	gaa	aaa	aaa	gac	gtg	tcc	att	tcc	aga	ctg	cga	gag	gcc	ttt	tct	1299
138	Glu	Glu	Lys	Lys	Asp	Val	Ser	Ile	Ser	Arg	Leu	Arg	Glu	Ala	Phe	Ser	
139	410			415						420				425			
141	ctt	cgt	cac	aca	aca	gag	aac	aag	cct	cac	agc	cca	aag	act	cca	gaa	1347
142	Leu	Arg	His	Thr	Thr	Glu	Asn	Lys	Pro	His	Ser	Pro	Lys	Thr	Pro	Glu	
143	430			435						440							
145	cca	aga	agg	agc	cct	cta	gga	cag	aaa	agg	ggt	atg	ctg	tct	tct	agc	1395
146	Pro	Arg	Arg	Ser	Pro	Leu	Gly	Gln	Lys	Arg	Gly	Met	Leu	Ser	Ser	Ser	
147	445			450						455							
149	act	tca	ggt	gcc	atc	tct	gac	aaa	ggc	gtc	ctg	aga	cct	cag	aaa	gag	1443
150	Thr	Ser	Gly	Ala	Ile	Ser	Asp	Lys	Gly	Val	Leu	Arg	Pro	Gln	Lys	Glu	
151	460			465						470							
153	gca	gtg	agt	tcc	agt	cac	gga	ccc	agt	gac	cct	acg	gac	aga	gct	gag	1491
154	Ala	Val	Ser	Ser	Ser	His	Gly	Pro	Ser	Asp	Pro	Thr	Asp	Arg	Ala	Glu	
155	475			480						485							
157	gtg	gag	aag	gac	tcg	ggg	cac	ggc	agc	act	tcc	gtg	gat	tct	gag	ggg	1539
158	Val	Glu	Lys	Asp	Ser	Gly	His	Gly	Ser	Thr	Ser	Val	Asp	Ser	Glu	Gly	
159	490			495						500				505			
161	tcc	agc	atc	cca	gac	ggc	agt	cac	tgc	agc	agc	gag	tat	gct	gcc		1587
162	Phe	Ser	Ile	Pro	Asp	Thr	Gly	Ser	His	Cys	Ser	Ser	Glu	Tyr	Ala	Ala	
163	510			515						520							
165	agc	tcc	cca	ggg	gac	agg	ggc	tcg	cag	gaa	cat	gtg	gac	tct	cag	gag	1635
166	Ser	Ser	Pro	Gly	Asp	Arg	Gly	Ser	Gln	Glu	His	Val	Asp	Ser	Gln	Glu	
167	525			530						535							
169	aaa	gct	cct	gaa	act	gac	gac	tct	ttt	tca	gat	gtg	gac	tgc	cat	tca	1683
170	Lys	Ala	Pro	Glu	Thr	Asp	Asp	Ser	Phe	Ser	Asp	Val	Asp	Cys	His	Ser	
171	540			545						550							
173	aac	cag	gaa	gat	acc	gga	tgt	aaa	ttt	cga	gtt	ttg	cct	cag	cca	act	1731
174	Asn	Gln	Glu	Asp	Thr	Gly	Cys	Lys	Phe	Arg	Val	Leu	Pro	Gln	Pro	Thr	
175	555			560						565							
177	aat	ctc	gca	acc	cca	aac	aca	aag	cgt	ttt	aaa	aaa	gaa	gaa	att	ctt	1779
178	Asn	Leu	Ala	Thr	Pro	Asn	Thr	Lys	Arg	Phe	Lys	Lys	Glu	Glu	Ile	Leu	
179	570			575						580				585			
181	tcc	agt	tct	gac	att	tgt	caa	aag	tta	gta	aat	act	cag	gac	atg	tca	1827
182	Ser	Ser	Ser	Asp	Ile	Cys	Gln	Lys	Leu	Val	Asn	Thr	Gln	Asp	Met	Ser	
183	590			595						600							
185	gcc	tct	cag	gtt	gat	gta	gct	gtg	aaa	att	aat	aag	aaa	gtt	gtg	ccc	1875
186	Ala	Ser	Gln	Val	Asp	Val	Ala	Val	Lys	Ile	Asn	Lys	Lys	Val	Val	Pro	
187	605			610						615							
189	ctg	gac	ttt	tct	atg	agt	tct	tta	gct	aaa	cga	ata	aag	cag	tta	cat	1923
190	Leu	Asp	Phe	Ser	Met	Ser	Ser	Leu	Ala	Lys	Arg	Ile	Lys	Gln	Leu	His	
191	620			625						630							
193	cat	gaa	gca	cag	caa	agt	gaa	ggg	gaa	cag	aat	tac	agg	aag	ttt	agg	1971

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194 His Glu Ala Gln Gln Ser Glu Gly Glu Gln Asn Tyr Arg Lys Phe Arg			
195 635	640	645	
197 gca aag att tgt cct gga gaa aat caa gca gcc gaa gat gaa cta aga		2019	
198 Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala Ala Glu Asp Glu Leu Arg			
199 650	655	660	665
201 aaa gag ata agt aaa acg atg ttt gca gaa atg gaa atc att ggt cag		2067	
202 Lys Glu Ile Ser Lys Thr Met Phe Ala Glu Met Glu Ile Ile Gly Gln			
203 670	675	680	
205 ttt aac ctg gga ttt ata ata acc aaa ctg aat gag gat atc ttc ata		2115	
206 Phe Asn Leu Gly Phe Ile Ile Thr Lys Leu Asn Glu Asp Ile Phe Ile			
207 685	690	695	
209 gtg gac cag cat gcc acg gac gag aag tat aac ttc gag atg ctg cag		2163	
210 Val Asp Gln His Ala Thr Asp Glu Lys Tyr Asn Phe Glu Met Leu Gln			
211 700	705	710	
213 cag cac acc gtg ctc cag ggg cag agg ctc ata gca cct cag act ctc		2211	
214 Gln His Thr Val Leu Gln Gly Gln Arg Leu Ile Ala Pro Gln Thr Leu			
215 715	720	725	
217 aac tta act gct gtt aat gaa gct gtt ctg ata gaa aat ctg gaa ata		2259	
218 Asn Leu Thr Ala Val Asn Glu Ala Val Leu Ile Glu Asn Leu Glu Ile			
219 730	735	740	745
221 ttt aga aag aat ggc ttt gat ttt gtt atc gat gaa aat gct cca gtc		2307	
222 Phe Arg Lys Asn Gly Phe Asp Phe Val Ile Asp Glu Asn Ala Pro Val			
223 750	755	760	
225 act gaa agg gct aaa ctg att tcc ttg cca act agt aaa aac tgg acc		2355	
226 Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro Thr Ser Lys Asn Trp Thr			
227 765	770	775	
229 ttc gga ccc cag gac gtc gat gaa ctg atc ttc atg ctg agc gac agc		2403	
230 Phe Gly Pro Gln Asp Val Asp Glu Leu Ile Phe Met Leu Ser Asp Ser			
231 780	785	790	
233 cct ggg gtc atg tgc cgg cct tcc cga gtc aag cag atg ttt gcc tcc		2451	
234 Pro Gly Val Met Cys Arg Pro Ser Arg Val Lys Gln Met Phe Ala Ser			
235 795	800	805	
237 aga gcc tgc cgg aag tcg gtg atg att ggg act gct ctt aac aca agc		2499	
238 Arg Ala Cys Arg Lys Ser Val Met Ile Gly Thr Ala Leu Asn Thr Ser			
239 810	815	820	825
241 gag atg aag aaa ctg atc acc cac atg ggg gag atg gac cac ccc tgg		2547	
242 Glu Met Lys Lys Leu Ile Thr His Met Gly Glu Met Asp His Pro Trp			
243 830	835	840	
245 aac tgt ccc cat gga agg cca acc atg aga cac atc gcc aac ctg ggt		2595	
246 Asn Cys Pro His Gly Arg Pro Thr Met Arg His Ile Ala Asn Leu Gly			
247 845	850	855	
249 gtc att tct cag aac tgaccgtagt cactgtatgg aataattggg tttatcgac		2650	
250 Val Ile Ser Gln Asn			
251 860			
253 attttatgt ttgaaagac agagtcttca ctaaccttt ttgtttaaa atgaaacctg		2710	
254 ctactaaaaa aaaatacaca tcacacccat ttaaaagtga tcttgagaac ctttcaaac		2770	
255 c			2771
257 <210> SEQ ID NO: 2			
258 <211> LENGTH: 862			

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259 <212> TYPE: PRT
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 2
263 Met Glu Arg Ala Glu Ser Ser Ser Thr Glu Pro Ala Lys Ala Ile Lys
264 1 5 10 15
265 Pro Ile Asp Arg Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Val
266 20 25 30
267 Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp
268 35 40 45
269 Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
270 50 55 60
271 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
272 65 70 75 80
273 Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
274 85 90 95
275 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
276 100 105 110
277 Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser
278 115 120 125
279 Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile
280 130 135 140
281 Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln
282 145 150 155 160
283 Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn
284 165 170 175
285 Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys
286 180 185 190
287 Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
288 195 200 205
289 Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys
290 210 215 220
291 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
292 225 230 235 240
293 Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly
294 245 250 255
295 Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe
296 260 265 270
297 Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln
298 275 280 285
299 Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg
300 290 295 300
301 Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
302 305 310 315 320
303 Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
304 325 330 335
305 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
306 340 345 350
307 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn
308 355 360 365

VERIFICATION SUMMARY

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